

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/734,782A
Source: IFw/b
Date Processed by STIC: 4/21/06

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/734,782A

DATE: 04/21/2006

TIME: 12:53:10

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\04212006\J734782A.raw

4 <110> APPLICANT: Griffiths, Steven
 5 Ritchie, Rachael Jane
 7 <120> TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences Of
 8 Infectious Salmon Anaemia Virus And Their Uses As Vaccines
 11 <130> FILE REFERENCE: H-32318B
 13 <140> CURRENT APPLICATION NUMBER: US 10/734,782A
 C--> 14 <141> CURRENT FILING DATE: 2004-04-02
 16 <150> PRIOR APPLICATION NUMBER: US 10/049,086
 17 <151> PRIOR FILING DATE: 2002-02-06
 19 <150> PRIOR APPLICATION NUMBER: PCT/GB00/02976
 20 <151> PRIOR FILING DATE: 2000-08-07
 22 <150> PRIOR APPLICATION NUMBER: GB 0006674.6
 23 <151> PRIOR FILING DATE: 2000-03-21
 25 <150> PRIOR APPLICATION NUMBER: GB 0005848.7
 26 <151> PRIOR FILING DATE: 2000-03-11
 28 <150> PRIOR APPLICATION NUMBER: GB 9918588.6
 29 <151> PRIOR FILING DATE: 1999-08-07
 31 <160> NUMBER OF SEQ ID NOS: 10
 33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 35 <210> SEQ ID NO: 1
 36 <211> LENGTH: 1821
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Infectious Salmon Anaemia Virus
 40 <400> SEQUENCE: 1
 41 caagatggat aacccgtg aatgcataaa ccgcaaaaga agactacttg ccttaccaga 60
 42 tggcctgaa acttcggat ccttctaaag tgatttgaga catctataca tgtgtgtgc 120
 43 tttctgtat caacacaaaa ccactggaga cgaatcaaga ttcaccaacc tggaaattact 180
 44 tgaccaagat gaagcactag gtccccaaag agctttgaa gccaaacatg gaataaaagg 240
 45 aggttcttta ggagacgttc ttgaccatga actgaaaaag gtcattgaat ttactttac 300
 46 ttctggaaat ttgtatattt ccgaacaaag aaaaagaaaag actcaagcag actaataat 360
 47 tgtgtgcgtt tcagaaggac ttaacgactt cagcgatca cacggagtgc tagacatggg 420
 48 acttgtggaa acaggggtga atgcagtaag agattctgc acacaaaacg gaataaccaat 480
 49 gaagataaat caggttagat ccacgagaac accaacacccg atcagcacat gcaaaatctc 540
 50 tgaacaaata acacgacaga taaacagtac aattactgaa aggaaaatgg aaacagtact 600
 51 ggcagcaatc gcaattaaac cagaactcaa actaactcag aaaggatgca gacccgtaa 660
 52 agaactagaa gatgaaaata ttctgtggat ggaccctcaa ttctgtgaaa ttgtatgaaag 720
 53 tttccttac agaggagggc catacggaa cttcctgcaa gaattgctgc ttacaaccaa 780
 54 cgacgttagag accaacccgg aagacagaga agaagtagta aagaagatac tggataacaa 840
 55 ggcgttccacc gttgaaagtgt gtgaatgcatt aataacactt ccagacaaaa tgacttgg 900
 56 cggagaacag gagaagaaga gaccagcaac aatagacgaa gtgagaaccg caggagaaag 960
 57 gttgaacag agtgttaaac cgaaaaccca aagatatgga aggttatcag acaaatggat 1020
 58 ggagcttggaa aagtttatct ttactgcaag caaaacagaa gtggatactt tccttctgt 1080
 59 agggaccgaa agacttgagt cgggtggagt gtgtgtcgga gctttacaca gagcgaccac 1140

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60 aaccaggata attagaccta tgattcaagg agggaaatgt tggggatga tttcaaaac 1200
 61 aaagtccaaa atggagaca cgaggaagga aggatactgt cacgcaatca tttcggaaa 1260
 62 agggaaagat aaatcaggac aaaacaagat gacaatgtg gggaaaacag tacattggca 1320
 63 tctaagacta gttaagtcta aaggagactg gatggcgcaa caactctgtg caaacaagg 1380
 64 cagaatatgg gaacatgacc ctgagctgt aacagaagga gtgacagtcc taatgacgcc 1440
 65 ttttctcag aaaattgcca ccattagtag atggagggca atgaggtagt acagcatgtt 1500
 66 tcatgtttct agtgcctggc atcattcacc tgcgtgtgaa gctgcatcg 1560
 67 aaagtttgcg gagatagtac atgcccataa ccagaaaaga gattgggtt 1620
 68 tatggaggac atggtaagg aagtggagga aataggggag cacttgcaga cggcatgtga 1680
 69 ttttagagtt tacaacatgt gcaaagcctt gattcagaaa attgcagtca gtacccaatg 1740
 70 agtggtttatt tacttgcataa ttgtgtgtg ttgacgata tgtatttgcg gacgcggccg 1800
 71 cggtcgacgc ggcgcgaat t 1821
 73 <210> SEQ ID NO: 2
 74 <211> LENGTH: 578
 75 <212> TYPE: PRT
 76 <213> ORGANISM: Infectious Salmon Anaemia Virus
 78 <400> SEQUENCE: 2
 79 Met Asp Asn Leu Arg Glu Cys Ile Asn Arg Lys Arg Arg Leu Leu Ala
 80 1 10 15
 81 Leu Pro Asp Val Pro Glu Thr Ser Asp Ala Phe Leu Ser Asp Leu Arg
 82 20 25 30
 83 His Leu Tyr Met Cys Val Ala Phe Cys Asp Gln His Lys Thr Thr Gly
 84 35 40 45
 85 Asp Glu Ser Arg Phe Thr Asn Leu Glu Leu Leu Asp Gln Asp Glu Ala
 86 50 55 60
 87 Leu Gly Ala Gln Arg Ala Phe Glu Ala Lys His Gly Ile Lys Gly Gly
 88 65 70 75 80
 89 Ser Leu Gly Asp Val Leu Asp His Glu Leu Lys Lys Val Ile Glu Phe
 90 85 90 95
 91 Thr Phe Thr Ser Gly Ser Leu Tyr Ile Ala Glu Gln Arg Lys Arg Lys
 92 100 105 110
 93 Thr Gln Ala Asp Ser Ile Ile Val Cys Val Ser Glu Gly Leu Asn Asp
 94 115 120 125
 95 Phe Ser Val Ser His Gly Val Leu Asp Met Gly Leu Val Glu Thr Gly
 96 130 135 140
 97 Val Asn Ala Val Arg Asp Phe Cys Thr Gln Asn Gly Ile Pro Met Lys
 98 145 150 155 160
 99 Ile Asn Gln Val Gly Ser Thr Arg Thr Pro Thr Pro Ile Ser Thr Cys
 100 165 170 175
 101 Lys Ile Ser Glu Gln Ile Thr Arg Gln Ile Asn Ser Thr Ile Thr Glu
 102 180 185 190
 103 Arg Lys Met Glu Thr Val Leu Ala Ala Ile Ala Ile Lys Pro Glu Leu
 104 195 200 205
 105 Lys Leu Thr Gln Lys Gly Cys Arg Pro Cys Lys Glu Leu Glu Asp Glu
 106 210 215 220
 107 Asn Ile Leu Trp Met Asp Pro Gln Phe Cys Glu Ile Asp Glu Ser Phe
 108 225 230 235 240
 109 Pro Tyr Arg Gly Gly Pro Tyr Gly Asn Phe Leu Gln Glu Leu Leu Leu
 110 245 250 255

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111 Thr Thr Asn Asp Val Glu Thr Asn Gly Lys Asp Arg Glu Glu Val Val
112 260 265 270
113 Lys Lys Ile Leu Asp Asn Lys Ala Phe Thr Val Glu Ser Gly Glu Cys
114 275 280 285
115 Ile Ile Thr Leu Pro Asp Lys Met Thr Cys Phe Gly Glu Gln Glu Lys
116 290 295 300
117 Lys Arg Pro Ala Thr Ile Asp Glu Val Arg Thr Ala Gly Glu Arg Phe
118 305 310 315 320
119 Glu Gln Ser Val Lys Pro Lys Thr Gln Arg Tyr Gly Arg Leu Ser Asp
120 325 330 335
121 Lys Trp Met Glu Leu Glu Lys Phe Ile Phe Thr Ala Ser Lys Thr Glu
122 340 345 350
123 Val Asp Thr Phe Leu Ser Val Gly Thr Glu Arg Leu Glu Ser Val Gly
124 355 360 365
125 Val Cys Val Gly Ala Leu His Arg Ala Thr Thr Thr Arg Ile Ile Arg
126 370 375 380
127 Pro Met Ile Gln Gly Lys Cys Trp Gly Met Met Phe Lys Thr Lys
128 385 390 395 400
129 Ser Lys Met Gly Asp Thr Arg Lys Glu Gly Tyr Cys His Ala Ile Ile
130 405 410 415
131 Phe Gly Lys Gly Glu Asp Lys Ser Gly Gln Asn Lys Met Thr Met Met
132 420 425 430
133 Gly Lys Thr Val His Trp His Leu Arg Val Val Lys Ser Lys Gly Asp
134 435 440 445
135 Trp Met Ala Gln Gln Leu Cys Ala Asn Lys Ser Arg Ile Trp Glu His
136 450 455 460
137 Asp Pro Glu Leu Val Thr Glu Gly Val Thr Val Leu Met Thr Pro Phe
138 465 470 475 480
139 Ser Gln Lys Ile Ala Thr Ile Ser Arg Trp Arg Ala Met Arg Leu Asp
140 485 490 495
141 Ser Met Phe His Val Ser Ser Ala Trp His His Ser Pro Ala Cys Glu
142 500 505 510
143 Ala Ala Ser Ala Met Leu Arg Lys Phe Val Glu Ile Val His Ala Ile
144 515 520 525
145 Asn Gln Lys Arg Asp Trp Gly Val Val Gly Ser Met Glu Asp Met Val
146 530 535 540
147 Lys Glu Val Glu Glu Ile Gly Glu His Leu Gln Thr Ala Cys Asp Phe
148 545 550 555 560
149 Arg Val Tyr Asn Met Cys Lys Ala Leu Ile Gln Lys Ile Ala Val Ser
150 565 570 575
151 Thr Gln
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 2018
157 <212> TYPE: DNA
158 <213> ORGANISM: Infectious Salmon Anaemia Virus
160 <400> SEQUENCE: 3
161 gcaaagatyg ctcaaattccc aaaaataata cagaaaaacgt ataagagatg gccgataaaag 60
162 gtatgactta ttcttttgat gtcagagaca acaccttggt tgtaagaaga tctaccgcta 120
163 ctaaaaagtgg cattaaagatc tcctacagag aggatcgagg aacatcactt ctccaaaagg 180

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164 cattcgccgg gacagaagat gaattctggg tggagttaga tcaagatgtc tacgttgaca 240
 165 aaaagattag aaaattcctg gaagaagaga aaatgaagga catgagcaca agagtgtctg 300
 166 gagcagtggc agcagcaatt gaaagatcag ttgaatttga caatttctca aaagaagcag 360
 167 cagctaacat tgaaatggct ggtgttagatg atgaagaagc tggaggaagt ggtctggtag 420
 168 acaacagaag gaagaacaaa ggggtctcaa acatggccta caatctgtct ctattcatag 480
 169 ggatggtgtt tcctgctctc actactttct tcagtgtat cctatcagaa ggtgaaatga 540
 170 gcatctggca aaatggacaa gcaatcatca gaattctggc actggcagat gaagacggaa 600
 171 agagacaaac aagaacagga ggacagaggg tggacatggc tgatgttaacc aagctgaacg 660
 172 tagtcacggc taacgggaaa gtcaagcaag ttgaagtaaa cttgaacat ctcaaagcag 720
 173 cattcaggca gatgacacct aaaagatcgg actacagaaa agggcaaggt tccaaggcta 780
 174 cagaatcaag catctccaac caatgtatgg cactgattat gaaatctgtc ctgtcagcag 840
 175 accaacttt tgctccggga gtgaagatga tgaggacgaa cggtttcaat gcgtcgtaca 900
 176 caacactggc agaaggggca aacattccga gcaagtacat aagacacatg aggaactgcg 960
 177 gaggagtagc tctggacctg atgggaatga agaggatcaa aaactcacct gaaggagcca 1020
 178 agtctaagat cttttccatc atccagaaga aagtaagagg aagatgtcgc acagaggagc 1080
 179 aacgcctccct gactagcgc ctgaaaatca ggcgcgtga aaacaagttc cagagaatca 1140
 180 tggacactct atgtacaagc ttctgtattt accctccaag aactacaaa tgcttcattc 1200
 181 cacctatttc cagtcctatg atgtacatcc aagaaggcaa ctctgtactg gcaatggatt 1260
 182 tcatgaaaaa cggagaggac gcctgcaga aactgcagaga agccaaactg aagtgagg 1320
 183 taaacagtac gttcacaatg tcagtagcta gaacatgcgt tgcaagtgtca atggttgc 1380
 184 cagcttttg ttctgcagat atcatcgaga atgcagtgc tgggtccgaa aggtacagat 1440
 185 ccaacatcaa ggctaacaca accaaaccaa aaaaggactc cacttacaca attcaaggac 1500
 186 ttagattgtc taacgtgagg tatgaagcaa gacgtgaaac atcacaaggc aacacagaca 1560
 187 gaagttggca agtgaacgtg actgacagct tcggaggact tgctgtttc aaccaagggg 1620
 188 caatttagaga aatgttagga gacggaaacat cagagacaac tagtgtaaac gtcagagccc 1680
 189 tggtaagag aattctgaaa tcagcttcag agaggagtgc aagagctgta aagacattta 1740
 190 tggtggaga acaagggaaa tcagctattt ttatctctgg tggggactg ttctctattt 1800
 191 actttgaagg ggttagaggaa gcgaaaagga taactgacat gacacctgaa attgagttt 1860
 192 acgaggacga cgaggaagag gaagacattt acatttagag tgacaattat gtaactttct 1920
 193 aattacccta tatttttga atatataatg aaactattttt gtgttaaagg ttgtgggttt 1980
 194 gattattaaa tttaaatttga aacggattt acgatattt 2018

196 <210> SEQ ID NO: 4

197 <211> LENGTH: 616

198 <212> TYPE: PRT

199 <213> ORGANISM: Infectious Salmon Anaemia Virus

201 <400> SEQUENCE: 4

202 Met Ala Asp Lys Gly Met Thr Tyr Ser Phe Asp Val Arg Asp Asn Thr
 203 1 5 10 15
 204 Leu Val Val Arg Arg Ser Thr Ala Thr Lys Ser Gly Ile Lys Ile Ser
 205 20 25 30
 206 Tyr Arg Glu Asp Arg Gly Thr Ser Leu Leu Gln Lys Ala Phe Ala Gly
 207 35 40 45
 208 Thr Glu Asp Glu Phe Trp Val Glu Leu Asp Gln Asp Val Tyr Val Asp
 209 50 55 60
 210 Lys Lys Ile Arg Lys Phe Leu Glu Glu Lys Met Lys Asp Met Ser
 211 65 70 75 80
 212 Thr Arg Val Ser Gly Ala Val Ala Ala Ile Glu Arg Ser Val Glu
 213 85 90 95
 214 Phe Asp Asn Phe Ser Lys Glu Ala Ala Asn Ile Glu Met Ala Gly

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215	100	105	110	
216	Val Asp Asp Glu Glu Ala Gly Gly Ser Gly Leu Val Asp Asn Arg Arg			
217	115	120	125	
218	Lys Asn Lys Gly Val Ser Asn Met Ala Tyr Asn Leu Ser Leu Phe Ile			
219	130	135	140	
220	Gly Met Val Phe Pro Ala Leu Thr Thr Phe Phe Ser Ala Ile Leu Ser			
221	145	150	155	160
222	Glu Gly Glu Met Ser Ile Trp Gln Asn Gly Gln Ala Ile Ile Arg Ile			
223	165	170	175	
224	Leu Ala Leu Ala Asp Glu Asp Gly Lys Arg Gln Thr Arg Thr Gly Gly			
225	180	185	190	
226	Gln Arg Val Asp Met Ala Asp Val Thr Lys Leu Asn Val Val Thr Ala			
227	195	200	205	
228	Asn Gly Lys Val Lys Gln Val Glu Val Asn Leu Asn Asp Leu Lys Ala			
229	210	215	220	
230	Ala Phe Arg Gln Ser Arg Pro Lys Arg Ser Asp Tyr Arg Lys Gly Gln			
231	225	230	235	240
232	Gly Ser Lys Ala Thr Glu Ser Ser Ile Ser Asn Gln Cys Met Ala Leu			
233	245	250	255	
234	Ile Met Lys Ser Val Leu Ser Ala Asp Gln Leu Phe Ala Pro Gly Val			
235	260	265	270	
236	Lys Met Met Arg Thr Asn Gly Phe Asn Ala Ser Tyr Thr Thr Leu Ala			
237	275	280	285	
238	Glu Gly Ala Asn Ile Pro Ser Lys Tyr Leu Arg His Met Arg Asn Cys			
239	290	295	300	
240	Gly Gly Val Ala Leu Asp Leu Met Gly Met Lys Arg Ile Lys Asn Ser			
241	305	310	315	320
242	Pro Glu Gly Ala Lys Ser Lys Ile Phe Ser Ile Ile Gln Lys Lys Val			
243	325	330	335	
244	Arg Gly Arg Cys Arg Thr Glu Glu Gln Arg Leu Leu Thr Ser Ala Leu			
245	340	345	350	
246	Lys Ile Ser Asp Gly Glu Asn Lys Phe Gln Arg Ile Met Asp Thr Leu			
247	355	360	365	
248	Cys Thr Ser Phe Leu Ile Asp Pro Pro Arg Thr Thr Lys Cys Phe Ile			
249	370	375	380	
250	Pro Pro Ile Ser Ser Leu Met Met Tyr Ile Gln Glu Gly Asn Ser Val			
251	385	390	395	400
252	Leu Ala Met Asp Phe Met Lys Asn Gly Glu Asp Ala Cys Lys Ile Cys			
253	405	410	415	
254	Arg Glu Ala Lys Leu Lys Val Gly Val Asn Ser Thr Phe Thr Met Ser			
255	420	425	430	
256	Val Ala Arg Thr Cys Val Ala Val Ser Met Val Ala Thr Ala Phe Cys			
257	435	440	445	
258	Ser Ala Asp Ile Ile Glu Asn Ala Val Pro Gly Ser Glu Arg Tyr Arg			
259	450	455	460	
260	Ser Asn Ile Lys Ala Asn Thr Thr Lys Pro Lys Lys Asp Ser Thr Tyr			
261	465	470	475	480
262	Thr Ile Gln Gly Leu Arg Leu Ser Asn Val Arg Tyr Glu Ala Arg Pro			
263	485	490	495	

VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date